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CORRESPONDENCE

The methodological 'revolution': caution accepted

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Porta and Bolúmar address the issue of 'overusing' new method developments in epidemiology at the expense of more classical and transparent methods [1]. They, thus, follow an old tradition of senior epidemiologists who question the need for and usefulness of new designs and new ways of analyzing data. Such a reaction is needed now as it has been in the past and it is warranted. This does not mean we should disregard these technical advancements—and Porta and Bolúmar do not state such a point of view themselves, but rather use a statement from one of the reviewers to advance this view. We should, however, use all the methods with care, and do all we can to understand the limitations of these methods—new and old. The *New England Journal of Medicine* (NEJM) was, for example, very quick to demand the use of multiple imputation rather than simple (old) methods to handle problems of missing data. The old methods were obviously limited and subject to bias but they were easy to understand and were usually interpreted with great care. More complicated methods may give the impression that selection bias is avoided by using a large number of fictitious data modelled using strong and often completely unrealistic assumptions.

Just notice how wrong opinion polls often are. Lack of respondents cannot be compensated for by modelling of how these non-respondents may have responded. Non-respondents are not refusing to answer at random, not even in the substrata we can generate by known characteristics of the non-respondents.

Porta and Bolúmar could have added one more plea from our past history, namely to present more raw data in published papers and more 'raw' and unadjusted associations. One of the important ideas behind Miettinen's confounder score [2] was the ability to present raw data on the association between the exposure and the disease, stratified on the estimated risk of getting the disease by using a limited number of strata (often 5). Results thus are not limited to statistical tests but are also presented by visual interpretation of sample size, number of observations in key strata, and so on; if adjusted results differ too much from unadjusted results, we need at least to understand why.

Our contribution to Porta and Bolúmar's commentary is a study based on simulations [3], and we would still advocate for this methodological option. Most epidemiologic studies are expensive and time consuming, and few epidemiologists will do more than a few studies in their lifetimes. Our experience in confounding and bias is thus limited. Making sampling and analyses of computer simulated data part of our breakfast ritual will substantially increase our understanding on how these sources of bias are generated.

The challenge is to maintain simplicity while at the same time advancing innovative new methods that capture new insights. New methods are clearly needed. Causation is complex; many diseases develop over long time periods, perhaps even over generations and often over several stages/steps that may have their own causal structure. We may not be able to imagine what would have happened to the exposed population had it not been exposed because the causal structure is too complicated and therefore this counterfactual thought experiment maybe too far from

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reality. The exposure may also be replaced with other exposures and effects be modified over the time course over stages of disease causation.

We may not yet have reached our limits in what we can achieve by our methods—old and new—but we should keep insisting on not making our analyses more complicated than needed. DAGs [4] illustrate a very useful set of rules for presenting causality in a simple but yet much more stringent way than what we have done before. New methods (as those presented in 3–5) [3–5] will find their place in our toolbox like they did in the past, when they have 'proved' their added value.

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